

REC'D PCT/PTO PATENT  
13 SEP 2001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

O. FAMODU ET AL.

CASE NO.: BB1270

APPLICATION NO.: 09/831,683

GROUP ART UNIT: UNKNOWN

INTERNATIONAL FILING DATE: 09 NOV 99 EXAMINER: UNKNOWN

FOR: PLANT AMINOACYL-tRNA SYNTHETASES

STATEMENT UNDER 37 CFR 1.821(g) and 1.825(b)

Assistant Commissioner for Patents  
Washington, DC 20231

Sir:

The submission of the substitute Sequence Listing filed concurrently herewith does not include new matter.

The copy of the substitute Sequence Listing in computer readable form filed concurrently herewith is the same as the paper copy of the substitute Sequence Listing filed concurrently herewith.

Respectfully submitted,



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Registration No. 41,272  
Telephone: 302-892-7760  
Facsimile: 302-892-1026

Dated: August 8, 2001

# SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company

<120> Plant Aminoacyl-tRNA Synthetases

<130> BB1270

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ttatcagatc gtccaaaccg gtggctctgt ttgcatccc agatggcagg cagcaggcct 2340  
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 tattgttgca ttgtacactt taatattgta ctgtgattag gctttactcg cggtggatgt 2460  
 ctttcaccgc tagatggcca gaggcataatc ctgccaacca agcagagcag ccattttgat 2520  
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 <211> 715  
 <212> PRT  
 <213> Zea mays

<400> 10  
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 1 5 10 15  
 Ile Cys Ala Ala Lys Leu Val Gly Leu Pro Leu Thr Ile Asn His Ser  
 20 25 30  
 Leu Ala Ala Gly Ser Ala Pro Thr Leu Gln Phe Ala Ser Gly Glu Ser  
 35 40 45  
 Leu His Gly Val Asn Pro Ile Ile Leu Tyr Ile Ala Arg Gly Ala Ser  
 50 55 60  
 Ile Ala Ser Leu Ser Gly Lys Asn Asp Ile Glu Phe Gly His Val Val  
 65 70 75 80  
 Glu Trp Leu Glu Tyr Ala Pro Thr Phe Leu Ser Gly Ser Glu Phe Glu  
 85 90 95  
 Asn Ala Cys Leu Phe Val Asp Gly Phe Leu Ala Ser Arg Thr Phe Leu  
 100 105 110  
 Val Gly His Gly Leu Thr Ile Ala Asp Ile Ala Val Trp Ser Asn Leu  
 115 120 125  
 Ala Gly Ile Gly Gln Arg Trp Glu Ser Leu Arg Lys Ser Lys Lys Tyr  
 130 135 140  
 Gln Asn Leu Val Arg Trp Phe Asn Ser Ile Asp Ser Glu Tyr Lys Glu  
 145 150 155 160  
 Ala Leu Asn Glu Val Val Ala Ala Phe Val Gly Lys Arg Gly Ile Gly  
 165 170 175  
 Lys Ser Pro Ala Pro Ser Leu Lys Glu Lys Val His Asp Ser Lys Asp  
 180 185 190  
 Pro Ser Ala Pro Glu Val Asp Leu Pro Gly Ala Lys Val Gly Lys Val  
 195 200 205  
 Cys Val Arg Phe Ala Pro Glu Pro Ser Gly Tyr Leu His Ile Gly His  
 210 215 220  
 Ala Lys Ala Ala Leu Leu Asn Lys Tyr Phe Ala Glu Arg Tyr Gln Gly  
 225 230 235 240  
 Arg Leu Ile Val Arg Phe Asp Asp Thr Asn Pro Ser Lys Glu Ser Asn  
 245 250 255

Glu Phe Val Glu Asn Leu Leu Lys Asp Ile Glu Thr Leu Gly Ile Lys  
 260 265 270  
 Tyr Asp Ala Val Thr Tyr Thr Ser Asp Tyr Phe Pro Lys Leu Met Glu  
 275 280 285  
 Met Ala Glu Ser Leu Ile Lys Gln Gly Lys Ala Tyr Ile Asp Asp Thr  
 290 295 300  
 Pro Lys Glu Gln Met Arg Lys Glu Arg Met Asp Gly Ile Glu Ser Arg  
 305 310 315 320  
 Cys Arg Asn Asn Thr Val Glu Glu Asn Leu Ser Leu Trp Lys Glu Met  
 325 330 335  
 Val Asn Gly Thr Glu Arg Gly Met Gln Cys Cys Val Arg Gly Lys Leu  
 340 345 350  
 Asp Met Gln Asp Pro Asn Lys Ser Leu Arg Asp Pro Val Tyr Tyr Arg  
 355 360 365  
 Cys Asn Thr Asp Pro His His Arg Val Gly Ser Lys Tyr Lys Val Tyr  
 370 375 380  
 Pro Thr Tyr Asp Phe Ala Cys Pro Phe Val Asp Ala Leu Glu Gly Val  
 385 390 395 400  
 Thr His Ala Leu Arg Ser Ser Glu Tyr His Asp Arg Asn Ala Gln Tyr  
 405 410 415  
 Tyr Arg Ile Leu Gln Asp Met Gly Leu Arg Arg Val Glu Ile Tyr Glu  
 420 425 430  
 Phe Ser Arg Leu Asn Met Val Tyr Thr Leu Leu Ser Lys Arg Lys Leu  
 435 440 445  
 Leu Trp Phe Val Gln Asn Lys Lys Val Glu Asp Trp Thr Asp Pro Arg  
 450 455 460  
 Phe Pro Thr Val Gln Gly Ile Val Arg Arg Gly Leu Lys Val Glu Ala  
 465 470 475 480  
 Leu Ile Gln Phe Ile Leu Gln Gln Gly Ala Ser Lys Asn Leu Asn Leu  
 485 490 495  
 Met Glu Trp Asp Lys Leu Trp Thr Ile Asn Lys Lys Ile Ile Asp Pro  
 500 505 510  
 Val Cys Ala Arg His Thr Ala Val Leu Lys Asp Gln Arg Val Ile Phe  
 515 520 525  
 Thr Leu Thr Asn Gly Pro Glu Glu Pro Phe Val Arg Ile Leu Pro Arg  
 530 535 540  
 His Lys Lys Phe Glu Gly Ala Gly Lys Lys Ala Thr Thr Phe Ala Asn  
 545 550 555 560  
 Arg Ile Trp Leu Asp Tyr Ala Asp Ala Ala Ala Ile Asn Lys Gly Glu  
 565 570 575

Glu Val Thr Leu Met Asp Trp Gly Asn Ala Ile Val Lys Glu Ile Lys  
 580 585 590  
 Val Glu Ser Gly Val Ile Thr Glu Leu Val Gly Glu Leu His Leu Glu  
 595 600 605  
 Gly Ser Val Lys Thr Thr Lys Leu Lys Ile Thr Trp Leu Ala Asp Ile  
 610 615 620  
 Glu Glu Leu Val Pro Leu Ser Leu Val Glu Phe Asp Tyr Leu Ile Ser  
 625 630 635 640  
 Lys Lys Lys Leu Glu Glu Asp Glu Asp Phe Leu Asp Asn Leu Asn Pro  
 645 650 655  
 Cys Thr Arg Arg Glu Ile Pro Ala Leu Gly Asp Ala Asn Met Arg Asn  
 660 665 670  
 Ile Lys Arg Gly Glu Ile Ile Gln Leu Glu Arg Lys Gly Tyr Tyr Arg  
 675 680 685  
 Cys Asp Ala Pro Phe Ile Arg Ser Ser Lys Pro Val Val Leu Phe Ala  
 690 695 700  
 Ile Pro Asp Gly Arg Gln Gln Ala Ser Leu Ser  
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<210> 11  
 <211> 1920  
 <212> DNA  
 <213> Oryza sativa

<220>  
 <221> unsure  
 <222> (139)

<220>  
 <221> unsure  
 <222> (238)

<220>  
 <221> unsure  
 <222> (431)

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 cgtcgccgac ggcaacctcc acgtcggcgg cgcccgcacc gcgcacttca actacctntt 240  
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 caccaagaag tccgaggagg ccgtgctcag tgacctcgcc tggctcggcc ttgactggga 360  
 cgaaggcccg gatgtcggtg gggaatatgg gcccgatcgc cagtcggagc gcaattcgat 420  
 gtacaaacag natgccgaga agctgatgga gtctggggca gtctatcagt gcttttactc 480  
 cagtgaaggga cttgaacaga tgaaggaaac tgcaagcaga tgcaaccttc cacctgtata 540  
 cattggcaag tgggggactg cttcagatgc agaaatacaa caggagttag agaaggggac 600  
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 tcgtggtgag gtcagttgga acttagacac gcttggtgat ttcgtgatta tgagaagcaa 720  
 tggccagcca gtgtataact tctgtgtcac agttgatgat gctaccatgc gcattctctca 780  
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taaactgtct aaacgtcatg gggctacttc tgtgggacag tacaaagaga tgggctatatt 960  
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 gttcttcacc attgatgacc tagtggaata attcactata aatcgtgtca acaaaagtgg 1080  
 agcagtcttt gatgctgtaa aattaaaatg gatgaatgga caacatctaa gatcatttcc 1140  
 ccctgatgta ctcatacaaga gttttgagga tagatggaag gacacaggca ttctccagga 1200  
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 cactgatgct gacgcagccc tttcaaacct gttgtcgtat cccctccatg ctacattaag 1320  
 cagtgatgaa gctaaatctg tgggtgcaaga caagctttct gaggttgcac caggactcat 1380  
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 gaagtgggtg aaaatttttg gcaaatcact taaaagaaag ggaaagtcac tctttatgcc 1500  
 gctccgtgta ctgctgactg gcaagcttca tgggcctgac atgggcggca ccgtagtcc 1560  
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 cgagaggttc agaatcctga aggaggtgga gtgggagtc ctggtacagg agcaagagtc 1680  
 cccagctgaa actgccgttc ctgcttctcg ataggctgca agattcagat caatcaggga 1740  
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 catttctaca gttgtgagga aactatagtt tccggtttct gtagttaata aagcgggaatt 1860  
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<210> 12  
 <211> 555  
 <212> PRT  
 <213> *Oryza sativa*

<220>  
 <221> UNSURE  
 <222> (130)

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 His Leu Arg Arg Pro Ser Pro Ser Ala Pro Pro Pro Pro Arg Arg  
 20 25 30  
 His Arg Thr Ala Pro Ala Ala Arg Cys Gly Pro Val Arg Ala Val Ala  
 35 40 45  
 Asp Gly Asn Leu His Val Gly Gly Ala Arg Thr Ala His Phe Asn Tyr  
 50 55 60  
 Leu Phe Ala Arg Ser Lys Gly Gly Lys Phe Val Leu Arg Ile Glu Asp  
 65 70 75 80  
 Thr Asp Phe Glu Arg Ser Thr Lys Lys Ser Glu Glu Ala Val Leu Ser  
 85 90 95  
 Asp Leu Ala Trp Leu Gly Leu Asp Trp Asp Glu Gly Pro Asp Val Gly  
 100 105 110  
 Gly Glu Tyr Gly Pro Asp Arg Gln Ser Glu Arg Asn Ser Met Tyr Lys  
 115 120 125  
 Gln Xaa Ala Glu Lys Leu Met Glu Ser Gly Ala Val Tyr Gln Cys Phe  
 130 135 140  
 Tyr Ser Ser Glu Gly Leu Glu Gln Met Lys Glu Thr Ala Ser Arg Cys  
 145 150 155 160  
 Asn Leu Pro Pro Val Tyr Ile Gly Lys Trp Gly Thr Ala Ser Asp Ala  
 165 170 175

Glu	Ile	Gln	Gln	Glu	Leu	Glu	Lys	Gly	Thr	Pro	Tyr	Thr	Tyr	Arg	Phe		
			180					185						190			
Arg	Val	Pro	Lys	Glu	Gly	Ser	Leu	Lys	Ile	Asn	Asp	Leu	Ile	Arg	Gly		
		195					200					205					
Glu	Val	Ser	Trp	Asn	Leu	Asp	Thr	Leu	Gly	Asp	Phe	Val	Ile	Met	Arg		
	210					215					220						
Ser	Asn	Gly	Gln	Pro	Val	Tyr	Asn	Phe	Cys	Val	Thr	Val	Asp	Asp	Ala		
225					230					235					240		
Thr	Met	Arg	Ile	Ser	His	Val	Ile	Arg	Ala	Glu	Glu	His	Leu	Pro	Asn		
				245					250					255			
Thr	Leu	Arg	Gln	Ala	Leu	Ile	Tyr	Lys	Ala	Leu	Gly	Phe	Pro	Met	Pro		
			260					265					270				
Ser	Phe	Ala	His	Val	Ser	Leu	Ile	Leu	Ala	Pro	Asp	Arg	Ser	Lys	Leu		
	275						280					285					
Ser	Lys	Arg	His	Gly	Ala	Thr	Ser	Val	Gly	Gln	Tyr	Lys	Glu	Met	Gly		
	290					295					300						
Tyr	Leu	Pro	Gln	Ala	Met	Val	Asn	Tyr	Leu	Ala	Leu	Leu	Gly	Trp	Gly		
305					310					315					320		
Asp	Gly	Thr	Glu	Asn	Glu	Phe	Phe	Thr	Ile	Asp	Asp	Leu	Val	Glu	Lys		
				325					330					335			
Phe	Thr	Ile	Asn	Arg	Val	Asn	Lys	Ser	Gly	Ala	Val	Phe	Asp	Ala	Val		
			340				345						350				
Lys	Leu	Lys	Trp	Met	Asn	Gly	Gln	His	Leu	Arg	Ser	Phe	Pro	Pro	Asp		
		355					360					365					
Val	Leu	Ile	Lys	Ser	Phe	Glu	Asp	Arg	Trp	Lys	Asp	Thr	Gly	Ile	Leu		
	370					375					380						
Gln	Glu	Ser	Glu	Ser	Gly	Phe	Ala	Lys	Glu	Ala	Ala	Glu	Leu	Leu	Lys		
385					390					395					400		
Asp	Gly	Ile	Asp	Leu	Ile	Thr	Asp	Ala	Asp	Ala	Ala	Leu	Ser	Asn	Leu		
				405				410						415			
Leu	Ser	Tyr	Pro	Leu	His	Ala	Thr	Leu	Ser	Ser	Asp	Glu	Ala	Lys	Ser		
			420					425					430				
Val	Val	Gln	Asp	Lys	Leu	Ser	Glu	Val	Ala	Ser	Gly	Leu	Ile	Ser	Ala		
		435					440					445					
Tyr	Asp	Ser	Gly	Glu	Leu	Cys	Gln	Ala	Leu	Ala	Glu	Gly	Arg	Asp	Gly		
	450					455					460						
Trp	Gln	Lys	Trp	Val	Lys	Ile	Phe	Gly	Lys	Ser	Leu	Lys	Arg	Lys	Gly		
465					470					475					480		
Lys	Ser	Leu	Phe	Met	Pro	Leu	Arg	Val	Leu	Leu	Thr	Gly	Lys	Leu	His		
				485					490					495			

Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys Ala Gly Thr  
500 505 510

Cys Gly Ala Val Thr Gln Gln Ser Gly Phe Val Asn Leu Asp Glu Arg  
515 520 525

Phe Arg Ile Leu Lys Glu Val Glu Trp Glu Ser Leu Val Gln Glu Gln  
530 535 540

Glu Ser Pro Ala Glu Thr Ala Val Pro Ala Ser  
545 550 555

<210> 13  
<211> 731  
<212> DNA  
<213> Glycine max

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tttctcaagt ctctgctctc tccgaacaac caccacccgt tcgcgttcgt ttcgctcctt 180  
ctcccaccgg aaacctccac gtcggcgggtg cccgaacggc cctcttcaac tacttggttcg 240  
caaggtccaa aggtgggaaa tttgtgctga gaattgagga cactgacttg gagaggtcca 300  
caagggagtc tgaggaggcc atgctcaaag atctttcttg gcttggactt gattgggatg 360  
aagggcctgg tgttgagggg gattatggtc cttataggca gtctgatagg aattctttat 420  
acaagcaatt tgcggataac ctacaccaat ccggtcatgt ttatcgctgc ttctgttcta 480  
atgaggaact agagaaaatg aaggaggatg ctaaactaaa gcaactgcct ccagtgtaca 540  
caggtaaatt ggccagtgc acaaatgagg aagtagaaga agagctagca aaaggaactc 600  
cttacactta ccggttccga gtccctaaag gaagtttaaa aattaatgat caaatacgag 660  
gcgaagttag ttggaacttg gatacgcttg gagattttgt gataatgagg agtaatggtc 720  
agcctgttta t 731

<210> 14  
<211> 404  
<212> PRT  
<213> Glycine max

<400> 14  
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20 25 30  
Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Ser Thr  
35 40 45  
Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu  
50 55 60  
Asp Trp Asp Glu Gly Pro Gly Val Gly Gly Asp Tyr Gly Pro Tyr Arg  
65 70 75 80  
Gln Ser Asp Arg Asn Ser Leu Tyr Lys Gln Phe Ala Asp Asn Leu His  
85 90 95  
Gln Ser Gly His Val Tyr Arg Cys Phe Cys Ser Asn Glu Glu Leu Glu  
100 105 110

Lys Met Lys Glu Asp Ala Lys Leu Lys Gln Leu Pro Pro Val Tyr Thr  
 115 120 125  
 Gly Lys Trp Ala Ser Ala Thr Asn Glu Glu Val Glu Glu Glu Leu Ala  
 130 135 140  
 Lys Gly Thr Pro Tyr Thr Tyr Arg Phe Arg Val Pro Lys Gly Ser Leu  
 145 150 155 160  
 Lys Ile Asn Asp Gln Ile Arg Gly Glu Val Ser Trp Asn Leu Asp Thr  
 165 170 175  
 Leu Gly Asp Phe Val Ile Met Arg Ser Asn Gly Gln Pro Val Tyr Asn  
 180 185 190  
 Phe Cys Val Thr Val Asp Asp Ala Thr Met Ala Ile Ser His Val Ile  
 195 200 205  
 Arg Ala Glu Glu His Leu Pro Asn Thr Leu Arg Gln Ala Leu Ile Tyr  
 210 215 220  
 Lys Ala Leu Gly Phe Pro Met Pro His Phe Ala His Val Ser Leu Ile  
 225 230 235 240  
 Leu Ala Pro Asp Arg Ser Lys Leu Ser Lys Arg His Gly Ala Thr Ser  
 245 250 255  
 Val Gly Gln Phe Arg Asp Met Gly Tyr Leu Pro Gln Ala Met Val Asn  
 260 265 270  
 Tyr Leu Ala Leu Leu Gly Trp Gly Asp Gly Thr Glu Asn Glu Phe Phe  
 275 280 285  
 Thr Leu Glu Gln Leu Val Glu Lys Phe Thr Ile Glu Arg Val Asn Lys  
 290 295 300  
 Ser Gly Ala Ile Phe Asp Ser Thr Lys Leu Arg Trp Met Asn Gly Gln  
 305 310 315 320  
 His Leu Arg Ser Leu Pro Ser Glu Glu Leu Asn Arg Ile Ile Gly Glu  
 325 330 335  
 Arg Trp Lys Asp Ala Gly Ile Ala Thr Glu Ser Gln Gly Ile Phe Ile  
 340 345 350  
 Gln Asp Ala Val Leu Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp  
 355 360 365  
 Ser Glu Lys Ala Leu Ser Ser Leu Leu Ser Tyr Pro Leu Tyr Glu Thr  
 370 375 380  
 Leu Ala Ser Ala Glu Gly Lys Pro Ile Leu Glu Asp Gly Val Ser Glu  
 385 390 395 400  
 Val Ala Lys Ser

<210> 15  
 <211> 407



<212> DNA  
<213> Triticum aestivum

<220>  
<221> unsure  
<222> (14)

<220>  
<221> unsure  
<222> (250)

<220>  
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gcaaggacgc gattcgcgcc gtcaccaaca gggaatcttc atcttggttc cctacgtacg 180  
gccctcttca attacctgat tgcaaaagct acacgcggta aattcatcct acgcatagag 240  
gacacagatn agtcaaggac tgttcctggt gcgattgaaa aactctgcgc tgntttgaga 300  
tggggggggt taaaaaggga taaaagggt ggtccccaat ngaccgcaan ngggcctttc 360  
aaaaatctca aaagactttt aangttataa aaaaaaacnc nccataa 407

<210> 16  
<211> 79  
<212> PRT  
<213> Triticum aestivum

<220>  
<221> UNSURE  
<222> (55)

<220>  
<221> UNSURE  
<222> (69)

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1 5 10 15

Ala Pro Ser Pro Thr Gly Asn Leu His Leu Gly Ser Leu Arg Thr Ala  
20 25 30

Leu Phe Asn Tyr Leu Ile Ala Lys Ala Thr Arg Gly Lys Phe Ile Leu  
35 40 45

Arg Ile Glu Asp Thr Asp Xaa Ser Arg Thr Val Pro Gly Ala Ile Glu  
50 55 60

Lys Leu Cys Ala Xaa Leu Arg Trp Gly Gly Leu Lys Arg Asp Lys  
65 70 75

<210> 17  
<211> 2387  
<212> DNA  
<213> Zea mays

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gcgggcgctg catgtcttaa tgcgcacga gctcaacgca cccgtcaaat tggggaagag 180  
ggatgctggt gaaaccggtg aggggaagga ggaggcactg gtggtgctgg ccacacagct 240  
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gaaggggatg cttgacaatg ttttgattga ttcagatgcc gtatcagtct tgaaggggt 420  
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gaagaagaaa actttgggta agggtaactt tgctgtgctc atgctgctta gggaccatgt 660  
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tctgtcattg ctatttgatc ccaaattgtcc aggattggag tcacttgtgg agaaggtgaa 780  
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caagatgcat ggtgctactg cgcttgatgc acccgattt gagctgagag aaacccttat 960  
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aagataccga gaattctacc aatgtgactt tgacattgct ggtgtatatg aacctatgga 1200  
accggatttt gaggtcataa aagttctgac tgaattgctg aatcagctgg atataggcac 1260  
atatgagata aaattaaatc acagaaagtt gcttgatggt atgttgagaa tttgtggtgt 1320  
gccccctcaa aagttcagaa cagtttgctc gagtattgac aaactggaca agcaaacatt 1380  
cgaacaggtg aagaaggaac tggttgatga gaaaggtata tcaaatgaaa ctgcggatga 1440  
aattggcaat ttagtgaaga ctaggggccc cccgttgga gttttgatgg agttgagaaa 1500  
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attattcaaa gctctggata aagcaaatgc aataagcaag ataacttttg atttaagttt 1620  
ggccaggggc cttgattact acactggtgt catatatgaa gccgttttca aggggtgcagc 1680  
tcaggttggc tccatagcgg ctggtggtcg gtacgacaac cttgtgggta tgtttagtgg 1740  
gaagcaaatc cctgctgttg gtgtgagcct tgggaattgag agagtctttg caatcatgga 1800  
gcagcaggag aaagaaagaa atgagaagat ccggcctaca gagacagagg tgctgggtgc 1860  
aattctggga aaggacctta ccctagctgc cgagctcggt agcgagctgt ggaatgctgg 1920  
gataaaggca gagttcaagc tcaactaccag ggtggcgaa cacaatcaagt atgccttgca 1980  
atcaagcatt ccgtggatgg tgctagtccg cgagcttgag ctgcagaaa gaaactgtaa 2040  
gttgaaggac gttgaagcca accaggaaga agaggtgat aggaaggatt ttgttcgaga 2100  
gttgaagaag agattgagta aatcctaaga ggaaaatttt aggcgttgat atcatctttt 2160  
gacaccatt tgacgcaaac tcaattaggg ggagaatgac attacatcat tataatttaa 2220  
actgacgtga atgtttcagt ccggttgga tagggccact tgttatgttc ataaggtcat 2280  
tcgaatcccc tgagtcccaa tgcattatgc tgatgaatca ggctgcagac atattgtgaa 2340  
ttatattctt tttgtactac cttgaggaat gaaaagtttt tgtcctc 2387

<210> 18  
 <211> 495  
 <212> PRT  
 <213> Zea mays

<400> 18

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Asn	Ser	Ala	Ser	Val	Ala	Glu	Trp	Ala	Thr	Ser	Leu	Ser	Leu	Leu	Phe
			20					25					30		
Asp	Pro	Lys	Cys	Pro	Gly	Leu	Glu	Ser	Leu	Val	Glu	Lys	Val	Lys	Glu
		35					40					45			
Ile	Val	Glu	Ser	Asn	Glu	Val	Arg	Arg	Leu	Pro	Lys	Ile	Pro	Lys	Gly
	50					55					60				
Thr	Arg	Asp	Phe	Gly	Lys	Glu	Gln	Met	Ala	Ile	Arg	Glu	Arg	Ala	Phe
65					70					75					80
Ser	Ile	Ile	Thr	Ser	Val	Phe	Lys	Met	His	Gly	Ala	Thr	Ala	Leu	Asp
				85					90					95	
Thr	Pro	Val	Phe	Glu	Leu	Arg	Glu	Thr	Leu	Met	Gly	Lys	Tyr	Gly	Glu
			100					105					110		
Asp	Ser	Lys	Leu	Ile	Tyr	Asp	Leu	Ala	Asp	Gln	Gly	Gly	Glu	Leu	Cys
		115					120					125			
Ser	Leu	Arg	Tyr	Asp	Leu	Thr	Val	Pro	Phe	Ala	Arg	Tyr	Val	Ala	Met
	130					135					140				
Asn	Ser	Ile	Ser	Ala	Leu	Lys	Arg	Tyr	Gln	Ile	Ala	Lys	Val	Tyr	Arg
145					150					155					160
Arg	Asp	Asn	Pro	Ser	Lys	Gly	Arg	Tyr	Arg	Glu	Phe	Tyr	Gln	Cys	Asp
				165					170					175	
Phe	Asp	Ile	Ala	Gly	Val	Tyr	Glu	Pro	Met	Glu	Pro	Asp	Phe	Glu	Val
			180					185					190		
Ile	Lys	Val	Leu	Thr	Glu	Leu	Leu	Asn	Gln	Leu	Asp	Ile	Gly	Thr	Tyr
		195					200					205			
Glu	Ile	Lys	Leu	Asn	His	Arg	Lys	Leu	Leu	Asp	Gly	Met	Leu	Glu	Ile
	210					215					220				
Cys	Gly	Val	Pro	Pro	Gln	Lys	Phe	Arg	Thr	Val	Cys	Ser	Ser	Ile	Asp
225					230					235					240
Lys	Leu	Asp	Lys	Gln	Thr	Phe	Glu	Gln	Val	Lys	Lys	Glu	Leu	Val	Asp
			245						250					255	
Glu	Lys	Gly	Ile	Ser	Asn	Glu	Thr	Ala	Asp	Glu	Ile	Gly	Asn	Leu	Val
			260					265					270		
Lys	Thr	Arg	Gly	Pro	Pro	Leu	Glu	Val	Leu	Met	Glu	Leu	Arg	Lys	Glu
		275					280					285			

Gly Ser Lys Phe Met Asn Asn Val Gly Ser Val Ala Ala Leu Asn Glu  
 290 295 300  
 Leu Glu Ile Leu Phe Lys Ala Leu Asp Lys Ala Asn Ala Ile Ser Lys  
 305 310 315 320  
 Ile Thr Phe Asp Leu Ser Leu Ala Arg Gly Leu Asp Tyr Tyr Thr Gly  
 325 330 335  
 Val Ile Tyr Glu Ala Val Phe Lys Gly Ala Ala Gln Val Gly Ser Ile  
 340 345 350  
 Ala Ala Gly Gly Arg Tyr Asp Asn Leu Val Gly Met Phe Ser Gly Lys  
 355 360 365  
 Gln Ile Pro Ala Val Gly Val Ser Leu Gly Ile Glu Arg Val Phe Ala  
 370 375 380  
 Ile Met Glu Gln Gln Glu Lys Glu Arg Asn Glu Lys Ile Arg Pro Thr  
 385 390 395 400  
 Glu Thr Glu Val Leu Val Ser Ile Leu Gly Lys Asp Leu Thr Leu Ala  
 405 410 415  
 Ala Glu Leu Val Ser Glu Leu Trp Asn Ala Gly Ile Lys Ala Glu Phe  
 420 425 430  
 Lys Leu Thr Thr Arg Val Ala Asn His Ile Lys Tyr Ala Leu Gln Ser  
 435 440 445  
 Ser Ile Pro Trp Met Val Leu Val Gly Glu Ser Glu Leu Gln Lys Gly  
 450 455 460  
 Thr Val Lys Leu Lys Asp Val Glu Ala Asn Gln Glu Glu Glu Val Asp  
 465 470 475 480  
 Arg Lys Asp Phe Val Arg Glu Leu Lys Lys Arg Leu Ser Lys Ser  
 485 490 495

<210> 19  
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 gtcgaaaggt tctgcaagaa gtattaaatt gttattcagt accagaaaat ttatttggca 180  
 aggtctgcgt cattattgat aaaattgaga aaattccagc tgacgagata aagaaagagt 240  
 tgaaagctgt tggctctatct caagaggctg tccaggagct attgcaagtc ctttctgtga 300  
 agtcattgac cgagttagaa gagagacttg ggagcagtg ggaagcagtt gctgatctga 360  
 aacagctatt ctcccttgct gaaaaaattg gttactctaa atggcttcaa tttgatgcat 420  
 cagttgttcg aggtcttgct tactacactg gcattgtatt tgagggtttt gaccgagaag 480  
 gaaagctgag agctatctgt ggtggtggc gatatgatca tttgttctca acttttgggtg 540  
 ctgatgacat tgctgcatgt ggttttggat ttggtgatgc aagtcatagt ggaattgctc 600  
 aaaagagaan ggtctgttac cgggaagctt aacttgcaaa tagatgacat tgtgtgtgcc 660  
 ttggaccaaa gatcttcaag ggatgtgctg ctatgggccc caacaatctc agngaaaaan 720  
 ggcaaattgt tgaagttggn tttgggaaaa caaa 754

<210> 20  
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 <212> PRT  
 <213> Glycine max

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 Ile Ala Ser Ile Val Thr Leu Phe Lys Arg Ile Gly Ile Thr Glu Ser  
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 Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu  
 35 40 45  
 Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile  
 50 55 60  
 Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu  
 65 70 75 80  
 Lys Ala Val Gly Leu Ser Gln Glu Ala Val Gln Glu Leu Leu Gln Val  
 85 90 95

Leu Ser Val Lys Ser Leu Thr Glu Leu Glu Glu Arg Leu Gly Ser Ser  
 100 105 110  
 Gly Glu Ala Val Ala Asp Leu Lys Gln Leu Phe Ser Leu Ala Glu Lys  
 115 120 125  
 Ile Gly Tyr Ser Lys Trp Leu Gln Phe Asp Ala Ser Val Val Arg Gly  
 130 135 140  
 Leu Ala Tyr Tyr Thr Gly Ile Val Phe Glu Gly Phe Asp Arg Glu Gly  
 145 150 155 160  
 Lys Leu Arg Ala Ile Cys Gly Gly Gly Arg Tyr Asp His Leu Phe Ser  
 165 170 175  
 Thr Phe Gly Ala Asp Asp Ile Ala Ala Cys Gly Phe Gly Phe Gly Asp  
 180 185 190  
 Ala Ser His Ser Gly Ile Ala Gln Lys Arg Xaa Val Cys Tyr Arg Glu  
 195 200 205  
 Ala Leu Ala Asn Arg His Cys Val Cys Leu Gly Pro Lys Ile Phe Lys  
 210 215 220  
 Gly Cys Ala Ala Met Gly Pro Asn Asn Leu Xaa Glu Lys Xaa Gln Ile  
 225 230 235 240  
 Val Glu Val

<210> 21  
 <211> 1164  
 <212> DNA  
 <213> Triticum aestivum

<400> 21  
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 tgacaagctg gggaaactga gtagggaaga aattgagaag gaattgattt caactgggct 180  
 gtcactctgaa gcagtacagg gcatcattga agtgctctct ctcaagtcac tgtccaaact 240  
 tgaagaggtg ctaggctcag gtgttgaagc cgttgctgac ttgaagaagc tcttctcgct 300  
 tgctgagcaa tatggttatt ctgattggat ctgtttcgat gcatctgttg ttcgtggcct 360  
 tgcatactac acagggattg tttttgaggc ttttgatagg gaaggggaac tgagagcgat 420  
 ttgtggtggg gggaggtatg acaggctact gtcaacattt ggaactgaag atgtaccagc 480  
 ctgtggcttt ggatttgag atgctgtcat agtggagctg ctgaaagaaa agggctcttt 540  
 gcctgacctg ccacgtcaaa tagatgacat tgtgttccca ttggacgagg agcttgaggg 600  
 gccagcatct agtgttgcat cctgtctgcg gaagaaggcg agatctgtag accttgtaga 660  
 agacaagcgt ctgaaatggg tgttcaaaca tgctgagagg ataaacgcta gcaggctgat 720  
 cttggttggg aaatccgagt gggagcgagg catggtccgt gtgaagatac tatcaaccag 780  
 agaagagttc gaggtcaagg cgggcgaatt gcagtagctg ttagctgatc tggctgattt 840  
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 ttcacgtcgt gtatacaaac aattaggtgg ctttgaatgc tattgccatc ttctttcgga 960  
 tcattcacct tgcaacaaac aaagaaattg taggttttgc cattcaccaa catgtattga 1020  
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 aaaaaaaaaa aaaaaaaaaa aaaa 1164

<210> 22  
 <211> 271

<212> PRT  
<213> Triticum aestivum

<400> 22

Lys Leu Gly Ile Thr Ser Ser Asp Val Gly Ile Arg Leu Ser Ser Arg  
1 5 10 15

Lys Val Leu Gln Ala Val Leu Asp Met Tyr Ser Val Pro Gln His Leu  
20 25 30

Phe Thr Gln Val Cys Val Ile Val Asp Lys Leu Gly Lys Leu Ser Arg  
35 40 45

Glu Glu Ile Glu Lys Glu Leu Ile Ser Thr Gly Leu Ser Ser Glu Ala  
50 55 60

Val Gln Gly Ile Ile Glu Val Leu Ser Leu Lys Ser Leu Ser Lys Leu  
65 70 75 80

Glu Glu Val Leu Gly Ser Gly Val Glu Ala Val Ala Asp Leu Lys Lys  
85 90 95

Leu Phe Ser Leu Ala Glu Gln Tyr Gly Tyr Ser Asp Trp Ile Cys Phe  
100 105 110

Asp Ala Ser Val Val Arg Gly Leu Ala Tyr Tyr Thr Gly Ile Val Phe  
115 120 125

Glu Ala Phe Asp Arg Glu Gly Glu Leu Arg Ala Ile Cys Gly Gly Gly  
130 135 140

Arg Tyr Asp Arg Leu Leu Ser Thr Phe Gly Thr Glu Asp Val Pro Ala  
145 150 155 160

Cys Gly Phe Gly Phe Gly Asp Ala Val Ile Val Glu Leu Leu Lys Glu  
165 170 175

Lys Gly Leu Leu Pro Asp Leu Pro Arg Gln Ile Asp Asp Ile Val Phe  
180 185 190

Pro Leu Asp Glu Glu Leu Glu Gly Pro Ala Ser Ser Val Ala Ser Cys  
195 200 205

Leu Arg Lys Lys Gly Arg Ser Val Asp Leu Val Glu Asp Lys Arg Leu  
210 215 220

Lys Trp Val Phe Lys His Ala Glu Arg Ile Asn Ala Ser Arg Leu Ile  
225 230 235 240

Leu Val Gly Lys Ser Glu Trp Glu Arg Gly Met Val Arg Val Lys Ile  
245 250 255

Leu Ser Thr Arg Glu Glu Phe Glu Val Lys Ala Gly Glu Leu Gln  
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<210> 23  
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 ttaagagtga tgggtggcttc aactatgcct caacagactt aactgctctt tggatcggc 180  
 tcaatgttga gcaggcagag tggatcatat atgttacaga tgttggtcag cagcagcact 240  
 ttgacatggt tttcagtgcg gcaaagatgg ccggttggtc cccagatcca agtgaaaaga 300  
 agttttccgaa aacaagccat gttggatttg gtcttgttct tggttcaaga tggcaagcgg 360  
 ttccgaaccc gcagtactga ggttggttcga ttggtagagc tacttgatga ggctaaatct 420  
 cggagcaaat cagaactact acaacggctc actgaaaatg gcaaaattgt tgactggacg 480  
 gatgangaat tagagcaaac ttcagaggct gttggatatg gtgctgtgaa gtacgctgat 540  
 ctaaaaaata acaggctcac taattacaca tttagttttg aacaaatgct gagcgataag 600  
 ggaaatactg ctgtgtacct tcagtatgca catgctcgta tttgttccat tattcggaaa 660  
 tccaacaaga acgtggnaga ctgaagagat ggagccattt ctctcgacca tccggattag 720  
 cgctgttggg gctgtatctt anccgatttg cagagttggt gaagaggatc acgaactact 780  
 ccaaatttgt gtgtgaatac tgtcaatcan ctgaaagtca caanatcata caactgcaag 840  
 tgggtgggtcc ngaggaacac cgggtgtgctt gcaacgacgc gtttcacna agnctcaccg 900  
 ctcggatacn cat 913

<210> 24  
 <211> 221  
 <212> PRT  
 <213> Zea mays



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 <222> (96)

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<400> 24

Phe Tyr Asn Pro Tyr Ile Pro Gln Val Leu Glu Glu Leu Ser Asn Lys  
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Gly Leu Ile Lys Glu Ser Glu Gly Ala Arg Val Ile Phe Ile Gln Gly  
 20 25 30

His Gln Ile Pro Leu Ile Val Val Lys Ser Asp Gly Gly Phe Asn Tyr  
 35 40 45

Ala Ser Thr Asp Leu Thr Ala Leu Trp Tyr Arg Leu Asn Val Glu Gln  
 50 55 60

Ala Glu Trp Ile Ile Tyr Val Thr Asp Val Gly Gln Gln Gln His Phe  
 65 70 75 80

Asp Met Val Phe Ser Ala Ala Lys Met Ala Gly Trp Leu Pro Asp Xaa  
 85 90 95

Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Phe Leu  
 100 105 110

Val Gln Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg  
 115 120 125

Leu Val Glu Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu Leu  
 130 135 140

Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Xaa Glu Leu Glu Gln  
 145 150 155 160

Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys Tyr Ala Asp Leu Lys  
 165 170 175

Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Glu Gln Met Leu Ser  
 180 185 190

Asp Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr Ala His Ala Arg Ile  
 195 200 205

Cys Ser Ile Ile Arg Lys Ser Asn Lys Asn Val Xaa Asp  
 210 215 220

<210> 25  
 <211> 551  
 <212> DNA  
 <213> Oryza sp.

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 ggttttgggg attaccagtg caacaatgct atgagtgtat tttcaagaat aagaggatcc 180  
 gcaacaaact tccgtaaccc catggcagtt gggcaggcaa ttgcaaataa cctccccag 240  
 tcaaataatta tcgaatccat ctctgttgcc ggantctggtt acattaacat aacgttatcc 300  
 agcaattgga ttgcacagag gatacaaaga catgcttggt tgtgggaatc aaaacatggg 360  
 gaacaatcct taacctgttt aagaaggcaa ntgctggntt tttcaanccc caataattgc 420  
 aaaaagaana tgcaagttgg gcaataatna aggncaacaa taaatngggg natancccaa 480  
 ctcaaaaangg ttngngntca caaaaanggtt aanttcntcn acgtaaacan gttgggaaac 540  
 nggggnacac a 551

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 <211> 68  
 <212> PRT  
 <213> Oryza sp.

<220>  
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 Arg Gly Ser Ala Thr Asn Phe Arg Asn Pro Met Ala Val Gly Gln Ala  
 20 25 30  
 Ile Ala Asn Asn Leu Pro Gln Ser Asn Ile Ile Glu Ser Ile Ser Val  
 35 40 45  
 Ala Gly Xaa Gly Tyr Ile Asn Ile Thr Leu Ser Ser Asn Trp Ile Ala  
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 Gln Arg Ile Gln  
 65

<210> 27  
 <211> 411

<212> DNA  
<213> Glycine max

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tatgttacag atattgggca gcaacagcac tttgatatnc tattnaaggc ctataggcgt 180  
gcaggttggt taccaaagga tgagaatgcg tatccaaaat gtactcatat aggttttggt 240  
cttggtcttg gggaagatgg aaaacgattt cggactcgca ncagtnangt tgttcgatta 300  
gttgattact tgatgaagct aaaangcgt gtaaaattgc cntcttgaaa cgtgatacaa 360  
ctaaaggatt ggnctgaagg aggagatcga gaaaacatcc gaagcagttg g 411

<210> 28  
<211> 115  
<212> PRT  
<213> Glycine max

<220>  
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<222> (6)

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<222> (96)

<220>  
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<222> (109)

<400> 28  
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Xaa Asn Tyr Phe Thr Thr Asp Leu Ala Ser Leu Trp Tyr Arg Leu Asn  
20 25 30  
Glu Glu Lys Leu Glu Trp Ile Val Tyr Val Thr Asp Ile Gly Gln Gln  
35 40 45  
Gln His Phe Asp Xaa Leu Xaa Lys Ala Tyr Arg Arg Ala Gly Trp Leu  
50 55 60  
Pro Lys Asp Glu Asn Ala Tyr Pro Lys Cys Thr His Ile Gly Phe Gly  
65 70 75 80  
Leu Val Leu Gly Glu Asp Gly Lys Arg Phe Arg Thr Arg Xaa Ser Xaa  
85 90 95  
Val Val Arg Leu Val Asp Tyr Leu Met Lys Leu Lys Xaa Ala Val Lys  
100 105 110  
Leu Pro Ser  
115

<210> 29  
<211> 565

<212> DNA  
<213> Triticum sp.

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<222> (350)

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caaaaacgag tcatgttggg tttggccttg ttcttggagc agatggcaag cgcttccgaa 120  
ctcgtagtagt tgaggttggt cggttgggaa gacctacttg atgaggctaa atctcgaagt 180  
aaatcaagaa cttctccaag cgtctcactg gaaaatggta aaattgttga ctggactgat 240  
gaaggaacta agagcaaact tcaaaaggca gtaagatatg gcgctgtcaa agtatgcggg 300  
tctgaaagaa taaccgactg actaattaca cttcaacttt gattcaagan ctaagtgaca 360  
agggaaatac tgctgtcnac ttcaataagc caagcccgtg cctcccanca ttcnaaaacc 420  
caacatgggtg tnnaaaacta aaangattgg anattccncc tgccanccaa atagctgcct 480  
gggacgnact aacngtatgc aanatgttaa aaggatgaca acncttccaa tgtcngggng 540  
aaactatnac tacnaagta aaagt 565

<210> 30  
<211> 33  
<212> PRT  
<213> Triticum sp.

<400> 30  
Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Val Leu  
1 5 10 15  
Gly Ala Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg  
20 25 30

Leu

<210> 31  
<211> 546  
<212> DNA  
<213> Oryza sp.

<220>  
<221> unsure  
<222> (448)

<220>  
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<400> 31  
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cattctccag gagtctgaaa gtggttttgc taaagaagcg gctgagcttt tgaaggatgg 120  
catcgatttg atcactgatg ctgacgcagc cctttcaaac ctgttgcgt atccctcca 180

tgctacatta agcagtgatg aagctaaatc tgtgggtgcaa gacaagcttt ctgaggttgc 240  
 atcaggactc atttctgctt atgatatcgg tgaactttgt caagcactag ctgagggccg 300  
 tgatgggttg cagaagtggg tgaataatc tggcaaatca cttaaaagaa agggaaaagtc 360  
 actctttatg ccgctccgtg tactgctgac tggcaagctt catgggcctg acatgggcgg 420  
 caccgtagtc ctcatacaca aagccggnac tgtggagcgg tcactcaaca atccgggttc 480  
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 aagatc 546

<210> 32  
 <211> 147  
 <212> PRT  
 <213> Oryza sp.

<400> 32  
 Pro Pro Asp Val Leu Ile Lys Ser Phe Glu Asp Arg Trp Lys Asp Thr  
 1 5 10 15  
 Gly Ile Leu Gln Glu Ser Glu Ser Gly Phe Ala Lys Glu Ala Ala Glu  
 20 25 30  
 Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp Ala Asp Ala Ala Leu  
 35 40 45  
 Ser Asn Leu Leu Ser Tyr Pro Leu His Ala Thr Leu Ser Ser Asp Glu  
 50 55 60  
 Ala Lys Ser Val Val Gln Asp Lys Leu Ser Glu Val Ala Ser Gly Leu  
 65 70 75 80  
 Ile Ser Ala Tyr Asp Ser Gly Glu Leu Cys Gln Ala Leu Ala Glu Gly  
 85 90 95  
 Arg Asp Gly Trp Gln Lys Trp Val Lys Ile Phe Gly Lys Ser Leu Lys  
 100 105 110  
 Arg Lys Gly Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly  
 115 120 125  
 Lys Leu His Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys  
 130 135 140  
 Ala Gly Thr  
 145

<210> 33  
 <211> 524  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> unsure  
 <222> (386)

<220>  
 <221> unsure  
 <222> (423)

<220>  
 <221> unsure  
 <222> (459)



<220>  
 <221> unsure  
 <222> (481)

<220>  
 <221> unsure  
 <222> (483)

<220>  
 <221> unsure  
 <222> (486)

<400> 33  
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 accactctca caccctcgc accttcttct tccaacgacg ccgtttctca gtctctgctc 120  
 tctccgaaca accaccaccc gttcgcgttc gtttcgctcc ttctcccacc ggaaacctcc 180  
 acgtcggcgg tgcccgaacg gccctcttca actacttggt cgcaagggtcc aaagggtggga 240  
 aatttgtgct gagaattgag gacactgact tggagagggt caagtaggga gtctgaggag 300  
 gccatgctca aagatcttct ttggcttggc cttgattggg atgaagggcc tgggtgttgg 360  
 aggggattat ggtccttaaa aggcantctg agaaggaatt ccttatacaa acaatatgcc 420  
 ggnгааacta cacaaatccg ggcaagttta accgctgcnt tctggtccaa agagggaact 480  
 nanagnaaat gaaaggaggt tgctaaacta aagcaactgg cccc 524

<210> 34  
 <211> 94  
 <212> PRT  
 <213> Glycine max

<220>  
 <221> UNSURE  
 <222> (63)

<400> 34  
 Gln Arg Arg Arg Phe Ser Val Ser Ala Leu Ser Glu Gln Pro Pro Pro  
 1 5 10 15  
 Val Arg Val Arg Phe Ala Pro Ser Pro Thr Gly Asn Leu His Val Gly  
 20 25 30  
 Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly  
 35 40 45  
 Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Xaa Ser  
 50 55 60  
 Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu  
 65 70 75 80  
 Asp Trp Asp Lys Gly Leu Gly Val Gly Gly Asp Tyr Gly Pro  
 85 90

<210> 35  
 <211> 506  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> unsure  
 <222> (18)

<220>  
 <221> unsure  
 <222> (483)

<220>  
 <221> unsure  
 <222> (505)

<220>  
 <221> unsure  
 <222> (506)

<400> 35  
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 tcgtcacttt gtttaagcga ataggaatta cagaatcaga tgtcggattt aagggttcca 120  
 gtcgaaaggt tctgcaagaa gtattaaatt gttattcagt accagaaaat ttatttggca 180  
 aggtctgcgt cattattgat aaaattgaga aaattccagc tgacgagata aagaaagagt 240  
 tgaaagctgt tggcttatct caagaggctg tccaggagct attgcaagtc ctttctgtga 300  
 agtcattgac cgagttagaa gagagacttg ggagagtggg gaagcagttg ctgatctgaa 360  
 acagtattct cccttgctga aaaaattggt tactctaaat gggttcaattt gatgatagtt 420  
 gttcgaggtc ttgcttacta cactggcatt gatttgaggg tttgacgaga ggaagctgca 480  
 gcntctgtgt gtgtcaatac attggn 506

<210> 36  
 <211> 48  
 <212> PRT  
 <213> Glycine max

<400> 36  
 Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu  
 1 5 10 15

Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile  
 20 25 30

Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu  
 35 40 45

<210> 37  
 <211> 577  
 <212> DNA  
 <213> Triticum sp.

<220>  
 <221> unsure  
 <222> (140)

<220>  
 <221> unsure  
 <222> (370)

<220>  
 <221> unsure  
 <222> (411)

<220>  
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 <222> (413)

<220>  
 <221> unsure  
 <222> (469)

<220>  
 <221> unsure  
 <222> (481)

<220>  
 <221> unsure  
 <222> (504)

<220>  
 <221> unsure  
 <222> (575)

<220>  
 <221> unsure  
 <222> (530)

<220>  
 <221> unsure  
 <222> (551)

<220>  
 <221> unsure  
 <222> (556)

<220>  
 <221> unsure  
 <222> (564)

<400> 37  
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 gtgtttggata tgtactccgt accacaacac ttgtttactc aagtttgtgt tattgttgac 120  
 aagctgggga aactgagtan ggaagaaatt gagaaggaat tgatttcaac tgggctgtca 180  
 tctgaagcag tacaggcat cattgaagt ctctctctca agtcactgtc caaacttgaa 240  
 gaggtgctag gctcaggtgt tgaagccgtt gctgacttga agaacctctt ctgccttgct 300  
 gagcaatatg gttattctga ttggatctgt ttgatgcat ctgttgttcg tggccttgca 360  
 tactacacan gggattgttt ttgaggcttt tgatagggaa gggaaactga nancatttgt 420  
 ggtggggggg aggtatgaca ggctacgtca acatttggaa ctgaagatnt ccaccctgtg 480  
 nctttggatt tggaatcctg tcanagtga ctcnnaaaga aaggtctttn ctacctgcac 540  
 tcaaataata nattgntcca ttgncaagac ttggggg 577

<210> 38  
 <211> 46  
 <212> PRT  
 <213> Triticum sp.

<220>  
 <221> UNSURE  
 <222> (38)

<400> 38  
 Ile Arg Leu Ser Ser Arg Lys Val Leu Gln Ala Val Leu Asp Met Tyr  
 1 5 10 15  
 Ser Val Pro Gln His Leu Phe Thr Gln Val Cys Val Ile Val Asp Lys  
 20 25 30

Leu Gly Lys Leu Ser Xaa Glu Glu Ile Glu Lys Glu Leu Ile  
35 40 45